

## REMARKS

Claims 1-2 and 6-19 are active in the present application. Support for Claims 15-19 is found in Claims 3-5 and the application as originally filed. No new matter is believed to have been added by these amendments. Applicants wish to thank Examiner Tung for indicating that Claims 10-14 are allowable over the prior art of record. In view of the amendments submitted and the following remarks favorable reconsideration and allowance of all pending claims is requested.

The rejection of Claims 1, 2, and 6-9 under 35 U.S.C. § 103(a) over Katsumata et al (Abstract) is respectfully traversed.

Katsumata et al disclose a *Corynebacterium* transformed with an *E. coli* citric acid synthase (CS) recombinant DNA or *Corynebacterium* transformed with a *Corynebacterium glutamicum* CS gene (see Abstract). However, Katsumata et al do not disclose or suggest an Enterobacteria having a coryneform CS gene as presently claimed. Notwithstanding this deficiency, the Examiner has alleged that based on the Katsumata disclosure, the skilled artisan would have an expectation of success by transforming other bacterial strains with the coryneform CS gene.

Applicants respectfully disagree and note that nothing in Katsumata suggests introducing a coryneform CS gene into an enterobacteria as claimed. Even assuming that the skilled artisan would have tried to transform an enterobacteria with the coryneform CS gene, such a skilled artisan would not have expected that L-glutamic acid production would be significantly better in bacterial strains transformed with a coryneform CS gene compared to the same bacterial strains transformed with a CS gene obtained from another source.

Applicants direct the Examiner's attention to Table 1 found on page 29 and reproduced below for convenience:

Table 1: Accumulated amount of L-glutamic acid

Bacterial Strain	Accumulated amount of L-glutamic acid (g/L)	Residual amount of Glucose (g/L)
AJ13355	0	0
AJ13355/pMWC	0.01	6.0
AJ13355/pMWCB	0.78	28.5
AJ13399	0	0
AJ13399/pMWC	2.85	0
AJ13399/pMWCB	4.71	0

In Table 1, AJ13355 is *Enterobacter agglomerans*, AJ13399 is *Klebsiella planticola*, pMWC is a plasmid with *E.coli gltA* and pMWCB is a plasmid with *Brevibacterium lactofermentum gltA* (see the specification on pages 27-28). The data in Table 1 clearly shows that L-glutamic acid production is significantly better when the bacterial strains are transformed with the *Brevibacterium lactofermentum gltA* (pMWCB) compared to the same bacterial strains transformed with *E.coli gltA*. Nothing in Katsumata suggests this improved L-glutamic acid production nor would one of skill in the art expect such an improvement based on the disclosure of Katsumata. Accordingly, withdrawal of this ground of rejection is requested.

The rejection of Claims 1, 6, 8 and 10 under 35 U.S.C. § 112, first paragraph (“enablement”) is respectfully traversed.

The Examiner has alleged that the specification does not enable an enterobacteria containing a DNA encoding any coryneform bacterial citrate synthase (page 2, paragraph 3 of the Official Action). The Examiner further alleges “[w]hile other bacterial citrate synthases are known, the prior art does not appear to teach any other coryneform bacterial citrate synthases besides *Corynebacterium glutamicum* and *Brevibacterium lactofermentum*.”

(Pages 2-3 of the Official Action). However, it appears that the Examiner has failed to appreciate the full scope Applicants' previous remarks and the reference provide. As stated on page 4 of Applicants' response:

This manuscript further describes amino acid sequences of citrate synthases from *E. coli*, *P. aeruginosa*, *R. prowazakii* and *Bacillus sp.* C4, and aligns these amino acid sequences revealing approximately seven highly conserved regions (see page 1824, right column, last paragraph). Therefore, coryneform bacterial citrate synthase genes other than the *Brevibacterium lactofermentum* gene can be cloned by conventional methods such as hybridization or PCR using fragments or oligonucleotides corresponding to the above conserved regions from bacterial chromosomal DNA.

Because the Applicants have described the isolation of the *gltA* gene by PCR using specific nucleotide primers shown in SEQ ID NOS:1 and 2 and methods of introducing the citrate synthase genes into bacteria (see pages 18-20), Applicants submit that the instant claims are clearly enabled by the specification as originally filed.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 1, 6, 8 and 10 under 35 U.S.C. § 112, first paragraph ("written description") is respectfully traversed.

The Examiner alleges that the specification does not provide a supporting disclosure for coryneform citrate synthase DNA other than *Brevibacterium lactofermentum* citrate synthase DNA based on the presumption that "the specification and claims do not indicate what distinguishing attributes are shared by members of the claimed genus of enterobacteria containing a citrate synthase gene derived from a coryneform bacteria." (Page 3 of the Official Action). Applicants respectfully disagree and point to the specification on page 4, line 11 to page 5, line 2, which states: "the inventors . . . have found it more effective, for enterobacteria, in improving L-glutamic acid productivity . . . to introduce a CS gene derived from a coryneform bacterium than to introduce a CS gene from a microorganism of the same

species as the enterobacteria." Therefore, the common distinguishing attribute shared by the claimed genus is the enterobacteria having a coryneform CS, which CS activity improves L-glutamic acid production in the bacteria. Accordingly, the present claims are deemed to be adequately described within the meaning of 35 U.S.C. § 112, first paragraph.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 1, 2 and 6-14 under 35 U.S.C. § 112, first paragraph is obviated by amendment.

Applicants submit that the present application is now in condition for allowance. Early notification of such allowance is earnestly solicited.

Respectfully submitted,

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IN THE CLAIMS

Please amend the claims as follows:

1. (Amended) A microorganism belonging to enterobacteria and having L-glutamic acid productivity, into which a DNA encoding a citrate synthase [gene] derived from a coryneform bacterium is introduced.

11. (Amended) A process for producing L-glutamic acid comprising isolating a DNA encoding a coryneform bacterium citrate synthase [gene] by amplifying the [gene] DNA with oligonucleotide primers prepared based on the nucleotide sequence of a *Corynebacterium glutamicum* citrate synthase gene [comprising SEQ ID NOS: 1 and 2];

transforming a enterobacteria with said isolated DNA encoding a citrate synthase [gene];

culturing said enterobacteria in a liquid medium to produce and accumulate the L-glutamic acid; and

collecting the L-glutamic acid produced.

Claims 15-19 (New).